International Livestock Research Institute

Training course report

Phylogenetic analysis of pathogens: “From faeces to phylogeny”

16-17 June 2014

CGIAR

ILRI
INTERNATIONAL LIVESTOCK RESEARCH INSTITUTE

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Project background

With a significant award from the Medical Research Council (UK)-coordinated program on the Environmental and Social Ecology of Human Infectious Diseases, itself funded through the UK Government's Living With Environmental Change Initiative, the Urban Zoonoses (UrbanZoo in short) project is undertaking a research program on the epidemiology, ecology and socio-economics of disease emergence in Nairobi.

The overall objective is to understand the mechanisms leading to the introduction of pathogens into urban populations through livestock commodity value chains, and their subsequent spread. The focus is on livestock as sources of these pathogens, because emerging diseases are likely to be zoonotic in origin, and livestock pathogens, through the close interactions between livestock, their products and people, are at high of risk crossing the species barrier. The focus in this project is on *Escherichia coli*, as an exemplar of many potential emerging pathogens, which exists in a diversity of hosts, in the environment, on food and in waste. The geographical focus is the city of Nairobi, Kenya and its hinterlands. In the microbiology components, the project takes a landscape genetics approach to understanding *E. coli* distribution and spread, with a view to understanding how this is affected by environmental and socio-economic factors.

The UrbanZoo project provides a unique opportunity to jointly analyse bacterial genome sequences alongside epidemiological data to understand the spread of bacteria between multiple hosts and sources. There is potential for several different sequencing projects on the Nairobi *E. coli* isolates. The spread of bacteria (geographically and between host species) could be investigated on different scales, such as between and within households, across Nairobi, and within the context of global strains and/or historical isolates.

Training summary

Organizer/co-organizers: Centre for Immunity, Infection and Evolution (CIIE) (http://ciie.bio.ed.ac.uk/) in conjunction with Eric Fèvre under the Urban Zoo project http://www.zoonotic-diseases.org/home/research/urbanzoonoses

Lecturer/facilitator: Dr. Melissa Ward, a CIIE research fellow

The training objective was to take the participants on a journey through the process of analysing pathogen genetic sequence data (for example, as will be generated from faecal samples in the UrbanZoo project) using molecular phylogenetics to test hypotheses about the spread of disease. It is a theory and practical course run by Melissa Ward of the University of Edinburgh and acting as an introduction to the theory of phylogenetic analysis and practical aspects of studies of genetic diversity and evolution.

Workshop participants attended lectures and computer-based practical sessions on using phylogenetics to understand the transmission of infectious disease between host species. The aim of the workshop was to show how state-of-the-art phylogenetic methods will be used to shed light on important source populations for bacterial disease in low-income areas of Nairobi and to equip participants with the skills to perform their own such analyses in the future. The workshop was attended by some 20 participants from the International Livestock Research Institute (ILRI), the Kenyan Medical Research Institute and the University of Nairobi.

Agenda

The workshop consisted of four half-day sessions over two days. Each session consisted of a one-hour lecture followed by a computer practical session for 1.5 to 2 hours. By the end of the workshop, participants were required to be able to manipulate genetic sequence data and produce and interpret phylogenetic trees from genetic sequences.

Session 1 – Genetic sequences

- Setting the scene – introduction to proposed phylogenetics work on the UrbanZoo data
- Introduction to genetic sequences and sequence assembly
- Manipulating and aligning genetic sequences

Session 2 – Introduction to phylogenetic trees

- Nucleotide substitution models and model selection
- Methods for constructing phylogenetic trees
- Manipulating and visualising phylogenetic trees

Session 3 – Understanding the spread of infectious disease (part 1)

- Testing phylogenetic support for a hypothesis
- Estimating emergence dates of strains from phylogenies
- Estimating rates of evolution from pathogen sequence data

Session 4 – Understanding the spread of infectious disease (part 2)

- Adding trait data (host species, geographical location) to phylogenies
- Phylogenetics for informing disease surveillance and control

The sessions were conducted according to the timetable below

DAY 1 – 16 June 2014	
Time	**Topic**
9:30 - 10:30	Lecture - genetic sequences
10:30 - 11:00	Tea/Coffee Break
11:00 - 12:30	Practical - genetic sequences
12:30 - 13:30	Lunch Break
13:30 - 14:30	Lecture - understanding phylogenies
14:30 - 16:00	Practical - understanding phylogenies
16:00	Tea/Coffee
DAY 2 – 17 June 2014	
Time	**Topic**
9:30 - 10:30	Lecture - constructing phylogenetics trees
10:30 - 11:00	Tea/Coffee Break
11:00 - 12:30	Lecture - infectious disease phylogenetics
12:30 - 13:30	Lunch Break
13:30 - 16:00	Practical - phylogenetics of infectious disease
16:00 - 17:00	Optional - time for participants to ask about their own proposed analyses
17:00	Tea/Coffee
CLOSE	

Training materials

Presentations https://www.dropbox.com/sh/peas66e9wev20hx/AADSMPWLWrGsutDjara59ajua

Practical sessions using an online program http://digitalworldbiology.com/dwb/BLAST

List of participants

The training was attended by 11 male and 11 female participants, all from Kenya

Serial No.	Name	Email contact	Sex (M/F)	Country of origin	Country Classification (Developing/Developed)
1	Cecilia Rumberia	C.rumberia@cgiar.org	F	Kenya	Developing
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* Trainer

Photos